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<120> ANTI-CD38 HUMAN ANTIBODIES AND USES THEREFOR

<130> 00361-8035.US00

<140> US 10/588,568
<141> 2006-08-04

<150> 60/541,911
<151> 2004-02-06

<150> 60/547,584
<151> 2004-02-26

<150> 60/553,943
<151> 2004-03-18

<150> 60/599,014
<151> 2004-08-06

<150> 60/614,471
<151> 2004-10-01

<160> 43

<170> PatentIn Ver. 3.3

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<400> 1
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gcggatagcg tgaaaggccg ttttaccatt tcacgtgata attcgaaaaa caccctgtat 240
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agctca 366

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<212> DNA
<213> Homo sapiens

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<210> 5
<211> 121
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
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Ser Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Asp Pro Asn Arg Gly Asn Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Tyr Ile Tyr Phe Ile His Gly Met Leu Asp Phe Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 6
<211> 122
<212> PRT
<213> Homo sapiens

<400> 6
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1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
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Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Asn Ile Arg Ser Asp Gly Ser Trp Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Arg Tyr Trp Ser Lys Ser His Ala Ser Val Thr Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 7
<211> 122
<212> PRT
<213> Homo sapiens

<400> 7

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ser Asn Ile Tyr Ser Asp Gly Ser Asn Thr Phe Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asn Met Tyr Arg Trp Pro Phe His Tyr Phe Phe Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 8
<211> 119
<212> PRT
<213> Homo sapiens

<400> 8

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Asn
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```
            20                  25                  30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
         35                  40                  45

Ser Asn Ile Ser Tyr Leu Ser Ser Ser Thr Tyr Tyr Ala Asp Ser Val
     50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Phe Tyr Gly Tyr Phe Asn Tyr Ala Asp Val Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser
        115
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<210> 9
<211> 342
<212> DNA
<213> Homo sapiens

<400> 9
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agtggggtcc cggatcgttt tagcggctct ggatccggca ccgattttac cctgaaaatt 240
agccgtgtgg aagctgaaga cgtgggcgtg tattattgcc agcagtattc ttctaagtct 300
gctacctttg gccagggtac gaaagttgaa attaaacgta cg 342

<210> 10
<211> 327
<212> DNA
<213> Homo sapiens

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ggtaaagcac cgaaactatt aatttataag gtttctaatt tgcaaagcgg ggtcccgtcc 180
cgttttagcg gctctggatc cggcactgat tttaccctga ccattagcag cctgcaacct 240
gaagactttg cgacttatta ttgccagcag gcttattctg gttctattac ctttggccag 300
ggtacgaaag ttgaaattaa acgtacg 327

<210> 11
<211> 324
<212> DNA
<213> Homo sapiens

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caggcgccag ttgttgtgat ttatggtgat aataatcgtc cctcaggcat cccggaacgc 180
tttagcggat ccaacagcgg caacaccgcg accctgacca ttagcggcac tcaggcggaa 240
gacgaagcgg attattattg ctcttcttat gattcttctt attttgtgtt tggcggcggc 300
acgaagttaa ccgttcttgg ccag 324

<210> 12

<211> 327
<212> DNA
<213> Homo sapiens

<400> 12
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tcgtgtagcg gcgataatat tggtcattat tatgcttctt ggtaccagca gaaacccggg 120
caggcgccag ttcttgtgat ttatcgtgat aatgatcgtc cctcaggcat cccggaacgc 180
tttagcggat ccaacagcgg caacaccgcg accctgacca ttagcggcac tcaggcggaa 240
gacgaagcgg attattattg ccagtcttat gattatcttc atgattttgt gtttggcggc 300
ggcacgaagt taaccgttct tggccag 327

<210> 13
<211> 114
<212> PRT
<213> Homo sapiens

<400> 13
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Phe Ile
20 25 30

Asp Gly Asn Asn Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Tyr
85 90 95

Ser Ser Lys Ser Ala Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr

<210> 14
<211> 109
<212> PRT
<213> Homo sapiens

<400> 14
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ala Phe
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Val Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Tyr Ser Gly Ser Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
            100                 105


<210> 15
<211> 108
<212> PRT
<213> Homo sapiens

<400> 15
Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
  1               5                  10                  15

Thr Ala Arg Ile Ser Cys Ser Gly Asp Asn Ile Gly Asn Lys Tyr Val
             20                  25                  30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Val Val Ile Tyr
         35                  40                  45

Gly Asp Asn Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
     50                  55                  60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
 65                  70                  75                  80

Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Asp Ser Ser Tyr Phe Val
                85                  90                  95

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
            100                 105


<210> 16
<211> 109
<212> PRT
<213> Homo sapiens

<400> 16
Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
  1               5                  10                  15

Thr Ala Arg Ile Ser Cys Ser Gly Asp Asn Ile Gly His Tyr Tyr Ala
             20                  25                  30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
         35                  40                  45

Arg Asp Asn Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
     50                  55                  60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
 65                  70                  75                  80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Leu His Asp Phe
                85                  90                  95

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
            100                 105
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<210> 17
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
consensus sequence

<400> 17
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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
  1               5                  10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
             20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
         35                  40                  45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
     50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                 85                  90                  95

Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 18
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
consensus sequence

<400> 18
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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
  1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
             20                  25                  30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
         35                  40                  45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
     50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                 85                  90                  95

Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
```

```
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 19
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      consensus sequence

<400> 19
Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
  1               5                  10                  15

Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala
             20                  25                  30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
         35                  40                  45

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
     50                  55                  60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
 65                  70                  75                  80

Asp Glu Ala Asp Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro Val
                 85                  90                  95

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105


<210> 20
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      consensus sequence

<400> 20
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
  1               5                  10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr
             20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
         35                  40                  45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
     50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro
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```
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210> 21
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      consensus sequence

<400> 21
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
  1               5                  10                  15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
             20                  25                  30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
         35                  40                  45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
     50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln His
                85                  90                  95

Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105                 110

Arg


<210> 22
<211> 300
<212> PRT
<213> Homo sapiens

<400> 22
Met Ala Asn Cys Glu Phe Ser Pro Val Ser Gly Asp Lys Pro Cys Cys
  1               5                  10                  15

Arg Leu Ser Arg Arg Ala Gln Leu Cys Leu Gly Val Ser Ile Leu Val
             20                  25                  30

Leu Ile Leu Val Val Val Leu Ala Val Val Val Pro Arg Trp Arg Gln
         35                  40                  45

Gln Trp Ser Gly Pro Gly Thr Thr Lys Arg Phe Pro Glu Thr Val Leu
     50                  55                  60

Ala Arg Cys Val Lys Tyr Thr Glu Ile His Pro Glu Met Arg His Val
 65                  70                  75                  80

Asp Cys Gln Ser Val Trp Asp Ala Phe Lys Gly Ala Phe Ile Ser Lys
                85                  90                  95
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His Pro Cys Asn Ile Thr Glu Glu Asp Tyr Gln Pro Leu Met Lys Leu
            100                 105                 110

Gly Thr Gln Thr Val Pro Cys Asn Lys Ile Leu Leu Trp Ser Arg Ile
        115                 120                 125

Lys Asp Leu Ala His Gln Phe Thr Gln Val Gln Arg Asp Met Phe Thr
    130                 135                 140

Leu Glu Asp Thr Leu Leu Gly Tyr Leu Ala Asp Asp Leu Thr Trp Cys
145                 150                 155                 160

Gly Glu Phe Asn Thr Ser Lys Ile Asn Tyr Gln Ser Cys Pro Asp Trp
                165                 170                 175

Arg Lys Asp Cys Ser Asn Asn Pro Val Ser Val Phe Trp Lys Thr Val
            180                 185                 190

Ser Arg Arg Phe Ala Glu Ala Ala Cys Asp Val Val His Val Met Leu
        195                 200                 205

Asn Gly Ser Arg Ser Lys Ile Phe Asp Lys Asn Ser Thr Phe Gly Ser
    210                 215                 220

Val Glu Val His Asn Leu Gln Pro Glu Lys Val Gln Thr Leu Glu Ala
225                 230                 235                 240

Trp Val Ile His Gly Gly Arg Glu Asp Ser Arg Asp Leu Cys Gln Asp
                245                 250                 255

Pro Thr Ile Lys Glu Leu Glu Ser Ile Ile Ser Lys Arg Asn Ile Gln
            260                 265                 270

Phe Ser Cys Lys Asn Ile Tyr Arg Pro Asp Lys Phe Leu Gln Cys Val
        275                 280                 285

Lys Asn Pro Glu Asp Ser Ser Cys Thr Ser Glu Ile
    290                 295                 300


<210> 23
<211> 1317
<212> DNA
<213> Homo sapiens

<400> 23
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tgcccagcac ctgaactcct gggggggaccg tcagtcttcc tcttcccccc aaaacccaag 720
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aagctcaccg tggacaagag caggtggcag caggggaacg tcttctcatg ctccgtgatg 1260
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<210> 24
<211> 642
<212> DNA
<213> Homo sapiens

<400> 24
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gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
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<210> 25
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 25
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<210> 26
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 26
tcagatctca gatgtgcaag atgaatc 27

<210> 27
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 27
ttggtaccag gtggcgccag cagtg 25

<210> 28
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 28
ttggtaccat ggccaactgc gag 23

<210> 29
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 29
ccgatatcag atctcagatg tgcaagatg 29

<210> 30
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 30
ccgatatcga tctcagatgt gcaagatg 28

<210> 31
<211> 363
<212> DNA
<213> Homo sapiens

<400> 31
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cctgggcagg gtctcgagtg gatgggctat atcgatccga atcgtggcaa tacgaattac 180
gcgcagaagt ttcagggccg ggtgaccatg acccgtgata ccagcattag caccgcgtat 240
atggaactga gcagcctgcg tagcgaagat acggccgtgt attattgcgc gcgtgagtat 300
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tca 363

<210> 32
<211> 1500
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic nucleotide construct

<220>
<221> CDS
<222> (307)..(393)

<400> 32
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actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc 120

aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg 180

gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca 240

ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gctggctagc 300

gccacc atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc 348
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro
1 5 10

aga tgg gtc ctg tcc cag gtg gaa ttc tgc agg cgg tta gct cag 393
Arg Trp Val Leu Ser Gln Val Glu Phe Cys Arg Arg Leu Ala Gln
15 20 25

cctccaccaa gggtccatcg gtcttccccc tggcaccctc ctccaagagc acctctgggg 453

gcacagcggc cctgggctgc ctggtcaagg actacttccc cgaaccggtg acggtgtcgt 513

ggaactcagg cgccctgacc agcggcgtgc acaccttccc ggctgtccta cagtcctcag 573

gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc acccagacct 633

acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaaa gttgagccca 693

aatcttgtga caaaactcac acatgcccac cgtgcccagc acctgaactc ctgggggggac 753

cgtcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc cggacccctg 813

aggtcacatg cgtggtggtg gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt 873

acgtggacgg cgtggaggtg cataatgcca agacaaagcc gcgggaggag cagtacaaca 933

gcacgtaccg ggtggtcagc gtcctcaccg tcctgcacca ggactggctg aatggcaagg 993

agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa accatctcca 1053

aagccaaagg gcagccccga gaaccacagg tgtacaccct gcccccatcc cgggatgagc 1113

tgaccaagaa ccaggtcagc ctgacctgcc tggtcaaagg cttctatccc agcgacatcg 1173

ccgtggagtg ggagagcaat gggcagccgg agaacaacta caagaccacg cctcccgtgc 1233

tggactccga cggctccttc ttcctctaca gcaagctcac cgtggacaag agcaggtggc 1293

agcaggggaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac cactacacgc 1353

agaagagcct ctccctgtct ccgggtaaat gagggcccgt ttaaacccgc tgatcagcct 1413

cgactgtgcc ttctagttgc cagccatctg ttgtttgccc ctcccccgtg ccttccttga 1473

ccctggaagg tgccactccc actgtcc 1500

<210> 33
<211> 800
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<220>
<221> CDS
<222> (307)..(705)

<400> 33
tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg 60

actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc 120

aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg 180

gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca 240

ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gctggctagc 300

gccacc atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg 348
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp
1 5 10

atc tct ggt gcc tac ggg gat atc gtg atg att aaa cgt acg gtg gct 396
Ile Ser Gly Ala Tyr Gly Asp Ile Val Met Ile Lys Arg Thr Val Ala
15 20 25 30

gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa tct 444
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
35 40 45

gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga gag 492
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
50 55 60

gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac tcc 540
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
65 70 75

cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc ctc 588
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
80 85 90

agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa gtc 636
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
95 100 105 110

tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca aag 684
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
115 120 125

agc ttc aac agg gga gag tgt taggggcccg tttaaacccg ctgatcagcc 735
Ser Phe Asn Arg Gly Glu Cys
130

tcgactgtgc cttctagttg ccagccatct gttgtttgcc cctcccccgt gccttccttg 795

accct 800

<210> 34
<211> 800
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide construct

<220>
<221> CDS
<222> (307)..(384)

<220>
<221> CDS
<222> (386)..(712)

<400> 34
tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg 60

actcacgggg atttccaagt ctccacccca ttgacgtcaa tgggagtttg ttttggcacc 120

aaaatcaacg ggactttcca aaatgtcgta acaactccgc cccattgacg caaatgggcg 180

gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca 240

ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gctggctagc 300

gccacc atg gcc tgg gct ctg ctg ctc ctc acc ctc ctc act cag ggc 348
Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln Gly
1 5 10

aca gga tcc tgg gct gat atc gtg atg cac gaa gtt a acc gtc cta ggt 397
Thr Gly Ser Trp Ala Asp Ile Val Met His Glu Val Thr Val Leu Gly
15 20 25 30

cag ccc aag gct gcc ccc tcg gtc act ctg ttc ccg ccc tcc tct gag 445
Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
35 40 45

gag ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata agt gac ttc 493
Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
50 55 60

tac ccg gga gcc gtg aca gtg gcc tgg aag gga gat agc agc ccc gtc 541
Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Gly Asp Ser Ser Pro Val
65 70 75

aag gcg gga gtg gag acc acc aca ccc tcc aaa caa agc aac aac aag 589
Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
80 85 90

tac gcg gcc agc agc tat ctg agc ctg acg cct gag cag tgg aag tcc 637
Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
95 100 105 110

cac aga agc tac agc tgc cag gtc acg cat gaa ggg agc acc gtg gag 685
His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
115 120 125

aag aca gtg gcc cct aca gaa tgt tca taggggcccg tttaaacccg 732
Lys Thr Val Ala Pro Thr Glu Cys Ser

130 135

ctgatcagcc tcgactgtgc cttctagttg ccagccatct gttgtttgcc cctcccccgt 792

gccttcct 800

<210> 35
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 35
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Glu Phe Cys Arg Arg Leu Ala Gln Ala Ser Thr
20 25 30

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
35 40 45

Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
50 55 60

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
65 70 75 80

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
85 90 95

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys
100 105 110

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu
115 120 125

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
130 135 140

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
145 150 155 160

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
165 170 175

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
180 185 190

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
195 200 205

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
210 215 220

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
225 230 235 240

```
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
                245                 250                 255

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
            260                 265                 270

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
        275                 280                 285

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
    290                 295                 300

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
305                 310                 315                 320

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
                325                 330                 335

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
            340                 345                 350

Leu Ser Leu Ser Pro Gly Lys
        355
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<210> 36
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic protein construct

<400> 36

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Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
  1               5                  10                  15

Gly Ala Tyr Gly Asp Ile Val Met Ile Lys Arg Thr Val Ala Ala Pro
             20                  25                  30

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr
         35                  40                  45

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
     50                  55                  60

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
 65                  70                  75                  80

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
                 85                  90                  95

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
            100                 105                 110

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
        115                 120                 125

Asn Arg Gly Glu Cys
    130
```

<210> 37
<211> 135
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
protein construct

<400> 37
Met Ala Trp Ala Leu Leu Leu Leu Thr Leu Leu Thr Gln Gly Thr Gly
1 5 10 15

Ser Trp Ala Asp Ile Val Met His Glu Val Thr Val Leu Gly Gln Pro
20 25 30

Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
35 40 45

Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro
50 55 60

Gly Ala Val Thr Val Ala Trp Lys Gly Asp Ser Ser Pro Val Lys Ala
65 70 75 80

Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala
85 90 95

Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
100 105 110

Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
115 120 125

Val Ala Pro Thr Glu Cys Ser
130 135

<210> 38
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 38
Val Ser Arg Arg Phe Ala Glu Ala Ala Cys Asp Val Val His Val
1 5 10 15

<210> 39
<211> 15
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 39
Phe Leu Gln Cys Val Lys Asn Pro Glu Asp Ser Ser Cys Thr Ser
1 5 10 15

<210> 40
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 40
Cys Gln Ser Val Trp Asp Ala Phe Lys Gly Ala Phe Ile
1 5 10

<210> 41
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 41
Thr Trp Cys Gly Glu Phe Asn Thr Ser Lys Ile Asn Tyr
1 5 10

<210> 42
<211> 120
<212> PRT
<213> Homo sapiens

<400> 42
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln

```
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 43
<211> 113
<212> PRT
<213> Homo sapiens

<400> 43

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Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
  1               5                  10                  15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
             20                  25                  30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
         35                  40                  45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
     50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln His
                 85                  90                  95

Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110

Arg
```